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OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/942,935

DATE: 12/13/2001
TIME: 13:47:30

Input Set : A:\032301.216.seq.ST25.txt
Output Set: N:\CRF3\12132001\I942935.raw

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       3 <110> APPLICANT: Degussa AG
       5 <120> TITLE OF INVENTION: Nucleotide Sequences Coding for the sigM Gene
       7 <130> FILE REFERENCE: 000449 BT
C-->   9 <140> CURRENT APPLICATION NUMBER: US/09/942,935
C-->   9 <141> CURRENT FILING DATE: 2001-12-13
       9 <160> NUMBER OF SEQ ID NOS: 4
      11 <170> SOFTWARE: PatentIn version 3.1
      13 <210> SEQ ID NO: 1
      14 <211> LENGTH: 1211
      15 <212> TYPE: DNA
      16 <213> ORGANISM: Corynebacterium glutamicum
      18 <220> FEATURE:
      19 <221> NAME/KEY: CDS
      20 <222> LOCATION: (236)..(907)
      21 <223> OTHER INFORMATION:
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      25 gacaccaatc cacagatgca gatcgctgaa gtacaacttg ttggttggta aattacgcgt      60
      27 ttgtgattga cccccattaa ggtgcgcccg ccctcagttt cactaactga aggcgggcgt     120
      29 ttttaattta tatatagctt cagctcacag gtattttcca gaaagaagag ccctcaaagt     180
      31 atgtagcacc tcagcgacac ctcccacttg agtgggcgcc gagaagtatc tctca atg     238
      32                                                               Met
      33                                                                 1
      35 gaa aat ctg ccc ata cta agc cgc ata agg gat acg ggg tgt gtc cct     286
      36 Glu Asn Leu Pro Ile Leu Ser Arg Ile Arg Asp Thr Gly Cys Val Pro
      37              5                  10                  15
      39 caa cct gcg ggg gat ctt atg aca gta ctg cct aaa aac cat gac cta     334
      40 Gln Pro Ala Gly Asp Leu Met Thr Val Leu Pro Lys Asn His Asp Leu
      41              20                  25                  30
      43 agc gat acc caa ctc gtc aaa cag ttt ata tct ggc gac tcc agg gca     382
      44 Ser Asp Thr Gln Leu Val Lys Gln Phe Ile Ser Gly Asp Ser Arg Ala
      45      35                  40                  45
      47 ttt tcc acc atc att cac cgc cac gaa cga cat atg atg cag gca gcc     430
      48 Phe Ser Thr Ile Ile His Arg His Glu Arg His Met Met Gln Ala Ala
      49 50                  55                  60                  65
      51 aga aaa tac ggg cgg aaa cca gaa gac gcc caa gac att ctc caa gaa     478
      52 Arg Lys Tyr Gly Arg Lys Pro Glu Asp Ala Gln Asp Ile Leu Gln Glu
      53                  70                  75                  80
      55 gct ctc ttt cgc gcc agc cga aac atg cac ctt tat aga gca gaa gca     526
      56 Ala Leu Phe Arg Ala Ser Arg Asn Met His Leu Tyr Arg Ala Glu Ala
      57                  85                  90                  95
      59 gct ctc ggc acg tgg ctc cac aaa ctt gtc ctg aat agc ggc ttc gat     574
      60 Ala Leu Gly Thr Trp Leu His Lys Leu Val Leu Asn Ser Gly Phe Asp
      61              100                 105                 110
      63 tgg gct acc cac cgc tcc caa gta gaa ttc ccc atc ctt aac gaa cca     622
      64 Trp Ala Thr His Arg Ser Gln Val Glu Phe Pro Ile Leu Asn Glu Pro
      65      115                 120                 125
      67 aca atc gat tta gaa aaa gat cct cgc cta gcc acc gac ccc ttg ggc     670
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68  Thr Ile Asp Leu Glu Lys Asp Pro Arg Leu Ala Thr Asp Pro Leu Gly
69  130             135             140             145
71  tac ctc gat gtc gcc atg aca att cga tcc gcc atc gac caa tta cac    718
72  Tyr Leu Asp Val Ala Met Thr Ile Arg Ser Ala Ile Asp Gln Leu His
73              150             155             160
75  ccc gat caa cgc atc gcc tta ata ctt gtc gac ctc ggc ggc tac acc    766
76  Pro Asp Gln Arg Ile Ala Leu Ile Leu Val Asp Leu Gly Gly Tyr Thr
77              165             170             175
79  gta gaa gat gtg gcc gaa atc gaa gga atc aaa gta ggt acc gtt aaa    814
80  Val Glu Asp Val Ala Glu Ile Glu Gly Ile Lys Val Gly Thr Val Lys
81              180             185             190
83  tca cgc cga ggg cgc gca cgc aaa gcg ttg cgc gcc ctt tta cat gca    862
84  Ser Arg Arg Gly Arg Ala Arg Lys Ala Leu Arg Ala Leu Leu His Ala
85              195             200             205
87  gat ttc ttc ggg ccc gaa gat ggc tcc ata cag tgc gaa agc aac        907
88  Asp Phe Phe Gly Pro Glu Asp Gly Ser Ile Gln Cys Glu Ser Asn
89  210             215             220
91  tgatggaagt ttttcaaagt gtctgacgtt gaaaacggtg agttcacaac tagggtgaat    967
93  ggtgcacgtg atgctgcact tttacgttta ctactttgag ggaaacaatg tctgaagaac    1027
95  aatctgccgt agcaccaaag attcatgatg tcgccatcat cggctccggt ccagctggct    1087
97  ataccgcagc agtatatgca gcccgcgctg acctcaaccc catcatgttc gagggctatg    1147
99  aatacggtgg atctttgatg accactactg acgtggaaaa cttcccaggc tttgaaaagg    1207
101 gaat                                                                1211
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 224
106 <212> TYPE: PRT
107 <213> ORGANISM: Corynebacterium glutamicum
109 <400> SEQUENCE: 2
111 Met Glu Asn Leu Pro Ile Leu Ser Arg Ile Arg Asp Thr Gly Cys Val
112 1               5               10              15
115 Pro Gln Pro Ala Gly Asp Leu Met Thr Val Leu Pro Lys Asn His Asp
116             20              25              30
119 Leu Ser Asp Thr Gln Leu Val Lys Gln Phe Ile Ser Gly Asp Ser Arg
120             35              40              45
123 Ala Phe Ser Thr Ile Ile His Arg His Glu Arg His Met Met Gln Ala
124     50              55              60
127 Ala Arg Lys Tyr Gly Arg Lys Pro Glu Asp Ala Gln Asp Ile Leu Gln
128 65              70              75              80
131 Glu Ala Leu Phe Arg Ala Ser Arg Asn Met His Leu Tyr Arg Ala Glu
132             85              90              95
135 Ala Ala Leu Gly Thr Trp Leu His Lys Leu Val Leu Asn Ser Gly Phe
136             100             105             110
139 Asp Trp Ala Thr His Arg Ser Gln Val Glu Phe Pro Ile Leu Asn Glu
140             115             120             125
143 Pro Thr Ile Asp Leu Glu Lys Asp Pro Arg Leu Ala Thr Asp Pro Leu
144     130             135             140
147 Gly Tyr Leu Asp Val Ala Met Thr Ile Arg Ser Ala Ile Asp Gln Leu
148 145             150             155             160
151 His Pro Asp Gln Arg Ile Ala Leu Ile Leu Val Asp Leu Gly Gly Tyr
```

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152                   165             170             175
155 Thr Val Glu Asp Val Ala Glu Ile Glu Gly Ile Lys Val Gly Thr Val
156                   180             185             190
159 Lys Ser Arg Arg Gly Arg Ala Arg Lys Ala Leu Arg Ala Leu Leu His
160           195             200             205
163 Ala Asp Phe Phe Gly Pro Glu Asp Gly Ser Ile Gln Cys Glu Ser Asn
164       210             215             220
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168 <211> LENGTH: 28
169 <212> TYPE: DNA
170 <213> ORGANISM: Corynebacterium glutamicum
172 <400> SEQUENCE: 3
173 caggtacctg gctacgagga cgattaag                                   28
176 <210> SEQ ID NO: 4
177 <211> LENGTH: 28
178 <212> TYPE: DNA
179 <213> ORGANISM: Corynebacterium glutamicum
181 <400> SEQUENCE: 4
182 tgtctagaaa gcatgcggag gaatcaac                                   28
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/942,935

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date